

Best Local Similarity 100.0%; Pred. No. 2.2e-285;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ATGACAACTCTCTAGATGATGAGACCTTTGGTACCACTCTCTATGATGACG 60
  |||
DB 1 ATGACAACTCTCTAGATGATGAGACCTTTGGTACCACTCTCTATGATGACG 60
OY 61 GGCCTGCTCTGTGAAAAGCTGATACAGAGCATGATGGCCAGTTTGGCCCGCTG 120
  |||
DB 61 GGCCTGCTCTGTGAAAAGCTGATACAGAGCATGATGGCCAGTTTGGCCCGCTG 120
OY 121 TACTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
  |||
DB 121 TACTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
OY 181 AATATCAGAGGCTCGAATTTATGACAACTCTCTCTCTCTCTCTCTCTCTCT 240
  |||
DB 181 AATATCAGAGGCTCGAATTTATGACAACTCTCTCTCTCTCTCTCTCTCTCT 240
OY 241 CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
  |||
DB 241 CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
OY 301 TTTGGCCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
  |||
DB 301 TTTGGCCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
OY 361 ATCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
  |||
DB 361 ATCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
OY 421 GGCCTTCTGAGCCCGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
  |||
DB 421 GGCCTTCTGAGCCCGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
OY 481 GAGAGCTGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
  |||
DB 481 GAGAGCTGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
OY 541 ACTCTTCTGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
  |||
DB 541 ACTCTTCTGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
OY 601 CTGAGATGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
  |||
DB 601 CTGAGATGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
OY 661 GGAATCATGAAAAGCTGCTGAGAGTCCCAAGTAAAAAAGTACAGAGCATCCGCTC 720
  |||
DB 661 GGAATCATGAAAAGCTGCTGAGAGTCCCAAGTAAAAAAGTACAGAGCATCCGCTC 720
OY 721 ATTTTCTGATCATGAGGCTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
  |||
DB 721 ATTTTCTGATCATGAGGCTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
OY 781 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
  |||
DB 781 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
OY 841 CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
  |||
DB 841 CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
OY 901 TACGCTTCTGAGAGAGGTTCCGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCT 960
  |||
DB 901 TACGCTTCTGAGAGAGGTTCCGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCT 960
OY 961 CTGATGACACCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
  |||
DB 961 CTGATGACACCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
OY 1021 TCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1065
  |||
DB 1021 TCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1065
```

DB 1021 TCTGCT 1065

# SEQUENCE USM PARISON

```
RESULT 2
US-08-575-967A-3
Sequence 3, Application US/08575967A
Patent No. 6265184
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1915 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 362..1426
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: /- "88-2B polynucleotide and amino acid
US-08-575-967A-3
```

Query Match 100.0%; Score 1065; DB 4; Length 1915;  
Best Local Similarity 100.0%; Pred. No. 2.7e-285;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ATGACAACTCTCTAGATGATGAGACCTTTGGTACCACTCTCTATGATGACG 60
  |||
DB 362 ATGACAACTCTCTAGATGATGAGACCTTTGGTACCACTCTCTATGATGACG 421
OY 61 GGCCTGCTCTGTGAAAAGCTGATACAGAGCATGATGGCCAGTTTGGCCCGCTG 120
  |||
DB 422 GGCCTGCTCTGTGAAAAGCTGATACAGAGCATGATGGCCAGTTTGGCCCGCTG 481
OY 121 TACTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
  |||
DB 482 TACTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
OY 181 AATATCAGAGGCTCGAATTTATGACAACTCTCTCTCTCTCTCTCTCTCTCTCT 240
  |||
DB 542 AATATCAGAGGCTCGAATTTATGACAACTCTCTCTCTCTCTCTCTCTCTCTCT 601
OY 241 CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
  |||
DB 602 CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 661
```

961 TC  
1021  
Feb 24 17:31:53 2003

us-09-922-895-2.rni

301 TTGGCCATGGCATGTAGTCTCTCAGGGTTTATACACAGGCTGTACAGCGAG 360  
662 TTGGCCATGGCATGTAGTCTCTCAGGGTTTATACACAGGCTGTACAGCGAG 721  
361 ATCTTTTATATATCTCTGTACAAATTCAGAGGTACCTGTGCTGTCTGTCT 420  
722 ATCTTTTATATATCTCTGTACAAATTCAGAGGTACCTGTGCTGTCTGTCT 781  
421 GCCCTTCAGCCGGAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 480  
782 GCCCTTCAGCCGGAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 841  
481 GCAGTGTACAGAGCTCTCTCTGAATTTATCTCTATGAGCTGAAGAGTTTGAAG 540  
842 GCAGTGTACAGAGCTCTCTCTGAATTTATCTCTATGAGCTGAAGAGTTTGAAG 901  
541 ACTCTTTGAGTGTCTTTTACCCAGAGATATAGTGTAGAGGATTTCCACT 600  
902 ACTCTTTGAGTGTCTTTTACCCAGAGATATAGTGTAGAGGATTTCCACT 961  
601 CTGAGATGACCATCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 660  
962 CTGAGATGACCATCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1021  
661 GGAATCATCAAAAGCGTCTGTAGAGTCCAGTAAAGGATACAGGCAATCCGGCTC 720  
1022 GGAATCATCAAAAGCGTCTGTAGAGTCCAGTAAAGGATACAGGCAATCCGGCTC 1081  
721 ATTTTGTATATAGGCGGTGTCTTTTATTTTGTGACACCTTACATGTGGTATCTT 780  
1082 ATTTTGTATATAGGCGGTGTCTTTTATTTTGTGACACCTTACATGTGGTATCTT 1141  
781 CTCTCTCTATCAATCAATCTTATTTGAAATGAGTGTAGAGGAGCAAGCATCTGGAG 840  
1142 CTCTCTCTATCAATCAATCTTATTTGAAATGAGTGTAGAGGAGCAAGCATCTGGAG 1201  
841 CTGCTATGCTGTGTAGAGAGTGTAGTCTCTCTCTCTCTCTCTCTCTCTCTCT 900  
1202 CTGCTATGCTGTGTAGAGAGTGTAGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1261  
901 TACGCTTTTGTGTAGAGAGTGTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960  
1262 TACGCTTTTGTGTAGAGAGTGTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1321  
961 CTCTACATCTGGGAGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020  
1322 CTCTACATCTGGGAGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1381  
1021 TCTGTCTCTCATCAAGAGAGCGGAACTCTCTATTTGTCTT 1065  
1382 TCTGTCTCTCATCAAGAGAGCGGAACTCTCTATTTGTCTT 1426

RESULT 3  
US-08-012-988A-1  
Sequence 1, Application US/08012988A  
Patent No. 5652133  
GENERAL INFORMATION:  
APPLICANT: Murphy, Philip M.  
TITLE OF INVENTION: Cloning and Expression of Human  
TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1)  
TITLE OF INVENTION: alpha/RANTES Receptor  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crek  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentlin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/012,988A  
FILING DATE: 19930128  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 15280-118  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2156 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 259..275  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 259..275  
FEATURE:  
NAME/KEY: complement (868..884)  
LOCATION:  
NAME/KEY: CDS  
LOCATION: 63..1128  
US-08-012-988A-1

Query Match 50.8%; Score 540.8; DB 1; Length 2156;  
Best Local Similarity 69.3%; Pred. No. 3.4e-140;  
Matches 737; Conservative 0; Mismatches 327; Indels 0; Gaps 0;  
1 ATGACACCTCACTAGATCACTTTGAGACCTTTGTTACACATCTCTATGATGACG 60  
63 ATGGAACCTCAAAACACAGAGAGTATGACACGACACAGATTGATGAGGAT 122  
61 GGCCTGCTGTGAAAGAGTATGACAGAGAGTATGAGGAGTATGAGGAGTATGAG 120  
123 GCACTTCCTGTCAGAGAGTATGAGAGAGGCTTTGGGAGGCTTGTGCTGCTG 182  
121 TACTCCCTGCTGTCTCTGAGGCTCTTGGGCAATGTGTGTGTATGATCTCTATA 180  
183 TACTCCCTGCTGTCTCTGAGGCTCTTGGGCAATGTGTGTGTATGATCTCTATA 242  
181 AATACAGAGAGTCTCCGAATATGACCAACATCTTACTGCTCAACTGGCATTTGGAG 240  
243 CAATACAGAGAGTCTCCGAATATGACCAACATCTTACTGCTCAACTGGCATTTGGAG 302  
241 CTGCTCTCTGCTGACAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
303 CTGCTCTCTGCTGACAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 362  
301 TTGGCCATGGCATGTAGTCTCTCAGGGTTTATACACAGGCTGTACAGCGAG 360  
363 TTGGCCATGGCATGTAGTCTCTCAGGGTTTATACACAGGCTGTACAGCGAG 422  
361 ATCTTTTATATATCTCTGTACAAATTCAGAGGTACCTGTGCTGTCTGTCTGT 420  
423 ATCTTTTATATATCTCTGTACAAATTCAGAGGTACCTGTGCTGTCTGTCTGT 482  
421 GCCCTTCAGCCGGAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 480  
483 GCCCTTCAGCCGGAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 542  
481 GCAGTGTACAGAGCTCTCTCTGAATTTATCTCTATGAGCTGAAGAGTTTGAAG 540  
543 GCAGTGTACAGAGCTCTCTCTGAATTTATCTCTATGAGCTGAAGAGTTTGAAG 602  
541 ACTCTTTGAGTGTCTTTTACCCAGAGATATAGTGTAGAGGATTTCCACT 600